REMARKS/ARGUMENTS

Claims 55-81 are pending. Favorable reconsideration is respectfully requested.

The present invention relates to a quantitative polymorphous analysis method, comprising:

determining the initial concentration of a target gene;

amplifying a target gene and monitoring the amplification by real-time PCR,

wherein said determining and amplifying are conducted at the same time;

performing a polymorphous analysis with respect to the amplified target gene to determine a polymorphous composition ratio of individual components of the target gene; and

determining the initial amount of the target gene and an initial polymorphous composition of the target gene or initial amounts of individual components of the target gene. See Claim 55.

The rejection of Claims 23-25 under 35 U.S.C. §102(b) over Liu et al. is respectfully traversed. Liu et al. fail to disclose the claimed method.

Liu et al. describe the characterization of microbial diversity by determining terminal restriction fragment length polymorphism of genes encoding the 16S RNA. See the Abstract.

Liu et al. do not describe a real-time PCR monitoring method. In addition, in the procedure described by the reference, the target gene is not determined accurately at the same time as the amplification of the target gene, and the initial amount or concentration of the target gene is not determined accurately. As a result, the results obtained by Liu et al. do not reflect the data before amplification. Instead, the data obtained are only a composition rate of each of the components.

Based on the foregoing, Liu et al. fail to disclose the claimed method. Accordingly, Claims 55-81 are not anticipated by that reference. Withdrawal of this ground of rejection is respectfully requested.

The rejection of Claims 23-25 under 35 U.S.C. §102(b) over Aynacioglu et al. is respectfully traversed.

Aynacioglu et al. describe the population frequency, mutation linkage and analytical methodology for different polymorphisms in a population. See the Abstract.

Aynacioglu et al. do not describe a real-time PCR monitoring method. In addition, in the procedure described by the reference, the target gene is not determined accurately at the same time as the amplification of the target gene, and the initial amount or concentration of the target gene is not determined accurately. As a result, the results obtained by Aynacioglu et al. do not reflect the data before amplification. Instead, the data obtained are only a composition rate of each of the components.

Based on the foregoing, Aynacioglu et al. fail to disclose the claimed method. Accordingly, Claims 55-81 are not anticipated by that reference. Withdrawal of this ground of rejection is respectfully requested.

The rejection of Claims 23-25 under 35 U.S.C. §102(b) over Zhang et al. is respectfully traversed.

Zhang et al. describe a *TSC*2 mutation in a patient with pulmonary tuberous sclerosis. See the Abstract.

Zhang et al. describe the population frequency, mutation linkage and analytical methodology for different polymorphisms in a population. See the Abstract.

Zhang et al. do not describe a real-time PCR monitoring method. In addition, in the procedure described by the reference, the target gene is not determined accurately at the same time as the amplification of the target gene, and the initial amount or concentration of the

target gene is not determined accurately. As a result, the results obtained by Zhang et al. do not reflect the data before amplification. Instead, the data obtained are only a composition rate of each of the components.

Based on the foregoing, Zhang et al. fail to disclose the claimed method. Accordingly, Claims 55-81 are not anticipated by that reference. Withdrawal of this ground of rejection is respectfully requested.

The rejection of Claims 23-25 under 35 U.S.C. §102(b) over Sreevatsan et al. is respectfully traversed.

Sreevatsan et al. describe an algorithmic approach to high-throughput molecular screening for alpha interferon-resistant genotypes in Hepatitis C patients. See the Abstract.

Sreevatsan et al. do not describe a real-time PCR monitoring method. In addition, in the procedure described by the reference, the target gene is not determined accurately at the same time as the amplification of the target gene, and the initial amount or concentration of the target gene is not determined accurately. As a result, the results obtained by Sreevatsan et al. do not reflect the data before amplification. Instead, the data obtained are only a composition rate of each of the components.

Based on the foregoing, Sreevatsan et al. fail to disclose the claimed method. Accordingly, Claims 55-81 are not anticipated by that reference. Withdrawal of this ground of rejection is respectfully requested.

The amendment to the substitute specification that were originally filed in the Preliminary Amendment on November 19, 2001 has been submitted herewith, expect that at page 66, "increase" has been replaced with –increase or decrease--. Support for all of the amendments is found in the substitute specification. In particular, the amendment at page 66 noted above is believed to be supported by the substitute specification at pages 6-7, where a decrease and an increase in emission are discussed.

The objection to the claims set forth at page 3 of the Official Action dated January 29, 2004 is believed to be obviated by the amendment submitted above.

The Restriction Requirement is believed to be moot, since the pending claims embrace the elected subject matter.

Applicants submit that the present application is in condition for allowance. Early notice to this effect is earnestly solicited.

Respectfully submitted,

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